RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Source: Parlo	Application Serial Number:	10/527,672	
D . D . 11 . cmr c	Source:	1 94/10	_
Date Processed by STIC: 3/24/05	Date Processed by STIC:	3/24/05	_

ENTERED



PCT

RAW SEQUENCE LISTING DATE: 03/24/2005
PATENT APPLICATION: US/10/527,672 TIME: 11:08:16

Input Set : A:\PP019766.0003 sequence listing.TXT

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4 <110> APPLICANT: Rappuoli, Rino
     6 <120> TITLE OF INVENTION: GROUP B STREPTOCOCCUS VACCINE
     9 <130> FILE REFERENCE: PP019766.0003
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/527,672
C--> 11 <141> CURRENT FILING DATE: 2005-03-11
     11 <150> PRIOR APPLICATION NUMBER: PCT/US2003/029167
    12 <151> PRIOR FILING DATE: 2003-09-15
    14 <150> PRIOR APPLICATION NUMBER: US 60/410,839
    15 <151> PRIOR FILING DATE: 2002-09-13
    17 <160> NUMBER OF SEQ ID NOS: 42
    19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
    21 <210> SEQ ID NO: 1
    22 <211> LENGTH: 1662
     23 <212> TYPE: DNA
    24 <213> ORGANISM: Streptococcus agalactiae
    26 <400> SEQUENCE: 1
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     27 atgaaattat cgaagaagtt attgttttcg gctgctgttt taacaatggt ggcggggtca
                                                                               120
     28 actqttqaac caqtaqctca qtttqcqact qqaatgagta ttgtaagagc tgcagaagtg
     29 tcacaagaac gcccagcgaa aacaacagta aatatctata aattacaagc tgatagttat
                                                                               180
     30 aaatcggaaa ttacttctaa tggtggtatc gagaataaag acggcgaagt aatatctaac
                                                                               240
                                                                               300
     31 tatqctaaac ttqqtqacaa tqtaaaaqqt ttqcaagqtg tacagtttaa acgttataaa
     32 gtcaagacgg atatttctgt tgatgaattg aaaaaattga caacagttga agcagcagat
                                                                               360
                                                                               420
     33 gcaaaagttg gaacgattct tgaagaaggt gtcagtctac ctcaaaaaac taatgctcaa
                                                                               480
     34 ggtttggtcg tcgatgctct ggattcaaaa agtaatgtga gatacttgta tgtagaagat
     35 ttaaaqaatt caccttcaaa cattaccaaa qcttatgctg taccgtttgt gttggaatta
                                                                               540
     36 ccagttgcta actctacagg tacaggtttc ctttctgaaa ttaatattta ccctaaaaac
                                                                               600
     37 qttgtaactg atgaaccaaa aacagataaa gatgttaaaa aattaggtca ggacgatgca
                                                                               660
                                                                               720
     38 ggttatacga ttggtgaaga attcaaatgg ttcttgaaat ctacaatccc tgccaattta
     39 ggtgactatg aaaaatttga aattactgat aaatttgcag atggcttgac ttataaatct
                                                                               780
     40 gttggaaaaa tcaagattgg ttcgaaaaca ctgaatagag atgagcacta cactattgat
                                                                               840
     41 qaaccaacag ttgataacca aaatacatta aaaattacgt ttaaaccaga gaaatttaaa
                                                                               900
     42 gaaattgctg agctacttaa aggaatgacc cttgttaaaa atcaagatgc tcttgataaa
                                                                               960
     43 gctactgcaa atacagatga tgcggcattt ttggaaattc cagttgcatc aactattaat
                                                                              1020
                                                                              1080
     44 gaaaaagcag ttttaggaaa agcaattgaa aatacttttg aacttcaata tgaccatact
     45 cctgataaag ctgacaatcc aaaaccatct aatcctccaa gaaaaccaga agttcatact
                                                                              1140
                                                                              1200
     46 ggtgggaaac gatttgtaaa gaaagactca acagaaacac aaacactagg tggtgctgag
     47 tttgatttgt tggcttctga tgggacagca gtaaaatgga cagatgctct tattaaagcg
                                                                              1260
     48 aatactaata aaaactatat tgctggagaa gctgttactg ggcaaccaat caaattgaaa
                                                                              1320
                                                                              1380
     49 tcacatacaq acqqtacqtt tqaqattaaa ggtttggctt atgcagttga tgcgaatgca
     50 gagggtacag cagtaactta caaattaaaa gaaacaaaag caccagaagg ttatgtaatc
                                                                              1440
                                                                              1500
     51 cctgataaag aaatcgagtt tacagtatca caaacatctt ataatacaaa accaactgac
                                                                              1560
     52 atcacqqttq ataqtqctqa tqcaacacct gatacaatta aaaacaacaa acgtccttca
                                                                              1620
     53 atccctaata ctggtggtat tggtacggct atctttgtcg ctatcggtgc tgcggtgatg
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Input Set : A:\PP019766.0003 sequence listing.TXT

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54 gcttttgctg ttaaggggat gaagcgtcgt acaaaagata ac
56 <210> SEQ ID NO: 2
57 <211> LENGTH: 554
58 <212> TYPE: PRT
59 <213> ORGANISM: Streptococcus agalactiae
61 <400> SEQUENCE: 2
62 Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
64 Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
66 Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
                               40
68 Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
70 Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
71 65
72 Tyr Ala Lys Leu Glý Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
74 Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
              100
                                   105
76 Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
          115
                               120
78 Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
                           135
                                               140
80 Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
                       150
                                           155
82 Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
                   165
                                       170
84 Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
               180
                                   185
86 Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
                               200
88 Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
                           215
90 Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
                       230
                                           235
92 Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
                                       250
                   245
94 Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
               260
96 Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
                               280
                                                   285
          275
98 Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu
                           295
100 Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
                        310
                                            315
102 Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
                    325
                                        330
104 Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr
```

Input Set : A:\PP019766.0003 sequence listing.TXT

105 340 345 350	
106 Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys	
107 355 360 365 108 Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg	
110 Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu	
111 385 390 395 400	
112 Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala	
113 405 410 415	
114 Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val	
115 420 425 430	
116 Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu	
117 435 440 445	
118 Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala	
119 450 455 460	
120 Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile	
121 465 470 475 480	
122 Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr	
123 485 490 495	
124 Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr	
125 500 505 510	
126 Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly Gly Ile Gly	
127 515 520 525	
128 Thr Ala Ile Phe Val Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val	
129 530 535 540	
130 Lys Gly Met Lys Arg Arg Thr Lys Asp Asn	
131 545 550	
133 <210> SEQ ID NO: 3	
134 <211> LENGTH: 1629	
135 <212> TYPE: DNA	
136 <213> ORGANISM: Streptococcus agalactiae	
138 <400> SEQUENCE: 3	
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140 ggtttagcat cagtaatttt agggtcattc ataatggtca caagtcctgt ttttgcgga	120
141 caaactacat cggttcaagt taataatcag acaggcacta gtgtggatgc taataattc	180
142 tccaatgaga caagtgcgtc aagtgtgatt acttccaata atgatagtgt tcaagcgtc	240
143 gataaagttg taaatagtca aaatacggca acaaaggaca ttactactcc tttagtaga	300
144 acaaagccaa tggtggaaaa aacattacct gaacaaggga attatgttta tagcaaaga	a 360
145 accgaggtga aaaatacacc ttcaaaatca gccccagtag ctttctatgc aaagaaagg	420
146 gataaagttt tctatgacca agtatttaat aaagataatg tgaaatggat ttcatataa	480
147 tetttttgtg gegtacgteg atacgeaget attgagteae tagateeate aggaggtte	
148 gagactaaag cacctactcc tgtaacaaat tcaggaagca ataatcaaga gaaaatagc	
149 acgcaaggaa attatacatt ttcacataaa gtagaagtaa aaaatgaagc taaggtagc	
150 agtccaactc aatttacatt ggacaaagga gacagaattt tttacgacca aatactaac	
151 attgaaggaa atcagtggtt atcttataaa tcattcaatg gtgttcgtcg ttttgtttt	
152 ctaggtaaag catcttcagt agaaaaaact gaagataaag aaaaagtgtc tcctcaacc	•
153 caagcccgta ttactaaaac tggtagactg actatttcta acgaaacaac tacaggttt	
154 gatatttaa ttacgaatat taaagatgat aacggtatcg ctgctgttaa ggtaccggt	
155 tggactgaac aaggaggca agatgatatt aaatggtata cagctgtaac tactgggga	
TIII CAAGCCAAAC AAAAAAAAAAAAAAAAAAAAAAAAA	. 1020

Input Set : A:\PP019766.0003 sequence listing.TXT

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156 ggcaactaca aagtagctgt atcatttgct gaccataaga atgagaaggg tctttataat
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157 attcatttat actaccaaga agctagtggg acacttgtag gtgtaacagg aactaaagtg
                                                                          1140
                                                                          1200
158 acagtagetg gaactaatte tteteaagaa eetattgaaa atggtttage aaagaetggt
159 qtttataata ttatcggaag tactgaagta aaaaatgaag ctaaaatatc aagtcagacc
                                                                          1260
160 caatttactt tagaaaaagg tgacaaaata aattatgatc aagtattgac agcagatggt
                                                                          1320
161 taccagtgga tttcttacaa atcttatagt ggtgttcgtc gctatattcc tgtgaaaaag
                                                                          1380
162 ctaactacaa gtagtgaaaa agcgaaagat gaggcgacta aaccgactag ttatcccaac
                                                                          1440
163 ttacctaaaa caggtaccta tacatttact aaaactgtag atgtgaaaag tcaacctaaa
                                                                          1500
                                                                          1560
164 gtatcaagtc cagtggaatt taattttcaa aagggtgaaa aaatacatta tgatcaagtg
                                                                          1620
165 ttagtagtag atggtcatca gtggatttca tacaagagtt attccggtat tcgtcgctat
166 attgaaatt
                                                                          1629
168 <210> SEQ ID NO: 4
169 <211> LENGTH: 543
170 <212> TYPE: PRT
171 <213> ORGANISM: Streptococcus agalactiae
173 <400> SEQUENCE: 4
174 Met Lys Lys Gly Gln Val Asn Asp Thr Lys Gln Ser Tyr Ser Leu Arg
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176 Lys Tyr Lys Phe Gly Leu Ala Ser Val Ile Leu Gly Ser Phe Ile Met
               20
                                    25
178 Val Thr Ser Pro Val Phe Ala Asp Gln Thr Thr Ser Val Gln Val Asn
            35
                                40
180 Asn Gln Thr Gly Thr Ser Val Asp Ala Asn Asn Ser Ser Asn Glu Thr
                            55
                                                60
182 Ser Ala Ser Ser Val Ile Thr Ser Asn Asn Asp Ser Val Gln Ala Ser
183 65
                        70
                                            75
184 Asp Lys Val Val Asn Ser Gln Asn Thr Ala Thr Lys Asp Ile Thr Thr
                                        90
186 Pro Leu Val Glu Thr Lys Pro Met Val Glu Lys Thr Leu Pro Glu Gln
                                    105
                100
187
188 Gly Asn Tyr Val Tyr Ser Lys Glu Thr Glu Val Lys Asn Thr Pro Ser
189
            115
                                120
190 Lys Ser Ala Pro Val Ala Phe Tyr Ala Lys Lys Gly Asp Lys Val Phe
        130
                            135
192 Tyr Asp Gln Val Phe Asn Lys Asp Asn Val Lys Trp Ile Ser Tyr Lys
                        150
                                            155
194 Ser Phe Cys Gly Val Arg Arg Tyr Ala Ala Ile Glu Ser Leu Asp Pro
                    165
                                        170
196 Ser Gly Gly Ser Glu Thr Lys Ala Pro Thr Pro Val Thr Asn Ser Gly
                180
                                    185
198 Ser Asn Asn Gln Glu Lys Ile Ala Thr Gln Gly Asn Tyr Thr Phe Ser
           195
                                200
                                                     205
200 His Lys Val Glu Val Lys Asn Glu Ala Lys Val Ala Ser Pro Thr Gln
                                                220
        210
                            215
202 Phe Thr Leu Asp Lys Gly Asp Arg Ile Phe Tyr Asp Gln Ile Leu Thr
                                            235
203 225
                        230
204 Ile Glu Gly Asn Gln Trp Leu Ser Tyr Lys Ser Phe Asn Gly Val Arg
                                        250
                    245
206 Arg Phe Val Leu Leu Gly Lys Ala Ser Ser Val Glu Lys Thr Glu Asp
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Input Set : A:\PP019766.0003 sequence listing.TXT

207				260					265					270			
208	Lys	Glu	Lys	Val	Ser	Pro	Gln	Pro	Gln	Ala	Arg	Ile	Thr	Lys	Thr	Gly	
209	_		275					280					285				
210	Arg	Leu	Thr	Ile	Ser	Asn	Glu	Thr	Thr	Thr	Gly	Phe	Asp	Ile	Leu	Ile	
211		290					295					300					
212	Thr	Asn	Ile	Lys	Asp	Asp	Asn	Gly	Ile	Ala	Ala	Val	Lys	Val	Pro	Val	
213	305					310					315					320	
214	Trp	Thr	Glu	Gln	Gly	Gly	Gln	Asp	Asp	Ile	Lys	Trp	Tyr	Thr	Ala	Val	
215					325					330					335		
216	Thr	Thr	Gly	Asp	Gly	Asn	Tyr	Lys	Val	Ala	Val	Ser	Phe	Ala	Asp	His	
217				340					345					350			
	Lys	Asn	Glu	Lys	Gly	Leu	Tyr		Ile	His	Leu	Tyr		Gln	Glu	Ala	
219			355					360					365	_	_	_	
220	Ser	_	Thr	Leu	Val	Gly		Thr	Gly	Thr	Lys		Thr	Val	Ala	Gly	
221		370					375					380		_	_•		
		Asn	Ser	Ser	Gln		Pro	Ile	Glu	Asn		Leu	Ala	Lys	Thr		
	385					390	_			_	395	_			_	400	
	Val	Tyr	Asn	Ile		Gly	Ser	Thr	Glu		Lys	Asn	Glu	Ala	Lys	Ile	
225	_	_			405			_		410		_	_		415	_	
	Ser	Ser	GIn		Gln	Phe	Thr	Leu		Lys	GLY	Asp	Lys		Asn	Tyr	
227	_	~3		420	een1		•	~1	425	61	m	- 1 -	0	430	T	0	
	Asp	GIN		ьeu	Thr	Ala	Asp	_	Tyr	GIN	Trp	тте		Tyr	Lys	Ser	
229	(The ease	Com	435	7707	71 ~~~	7~~	П	440	Dro	17-1	T	T	445	mh~	Thr	Cor	
	TYL	450	GIY	vai	Arg	Arg	191 455	116	PIO	vai	гуѕ	цу5 460	ьeu	1111	Thr	SET	
231	C02		Tarc	772	Tarc	λαν		λla	Thr	Larc	Dro		Sar	Туг	Pro	Δen	
	465	Giu	пуъ	AIA	пуъ	470	Giu	ALG	1111	цуь	475	1111	261	1 Y L	FIO	480	
		Pro	Lvc	Thr	Glv		Tvr	Thr	Phe	Thr		Thr	Val	Asp	Val		
235	пси	110	טעם	****	485		-1-		1110	490	27.0			1101	495	-10	
	Ser	Gln	Pro	Lvs		Ser	Ser	Pro	Val		Phe	Asn	Phe	Gln	Lys	Glv	
237	-00			500			-00		505					510	-1-	1	
	Glu	Lvs	Ile		Tvr	Asp	Gln	Val		Val	Val	Asp	Gly		Gln	Trp	
239			515		- 4			520				-	525			-	
	Ile	Ser	Tyr	Lys	Ser	Tyr	Ser	Gly	Ile	Arg	Arg	Tyr	Ile	Glu	Ile		
241		530	-	•		•	535	_		_	_	540					
243	<21	0 > S	EQ II	ON C	: 5												
244	<21	1> L	ENGT	H: 26	570												
245	<21	2> T	YPE:	DNA													
246	<213	3 > O	RGAN	ISM:	Str	epto	cocci	ıs aç	galad	ctia	e						
248	<40	0 > S	EQUE	NCE:	5												
249	atg	aaaa	aga 🤉	gacaa	aaaa	at at	tggag	gagg	g tta	atca	gtta	ctt	tacta	aat	cctgi	cccaa	60
																ggaaaa	120
251	gtaa	attgi	tta a	aaaaa	aacg	gg ag	gacaa	atgci	t aca	acca	ttag	gca	aagc	gac	tttt	gtgtta	180
252	aaaa	aatga	aca a	atgat	taagt	tc ag	gaaa	caagt	ca(cgaa	acgg	tag	aggg	ttc	tggag	gaagca	240
253	acct	tttg	aaa a	acata	aaaa	cc to	ggaga	acta	c aca	atta	agag	aag	aaac	agc .	accaa	attggt	300
																ataatc	360
																atcca	420
																ggttcc	480
257	aaa	gttg	gtg a	aacaa	ataca	aa ag	gcatt	gaat	t cca	aataa	aatg	gaa	aaga	tgg	tcgaa	agagag	540

Input Set : A:\PP019766.0003 sequence listing.TXT

Output Set: N:\CRF4\03242005\J527672.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:22; Xaa Pos. 240
Seq#:40; Xaa Pos. 281

VERIFICATION SUMMARY

DATE: 03/24/2005

PATENT APPLICATION: US/10/527,672

TIME: 11:08:17

Input Set : A:\PP019766.0003 sequence listing.TXT

Output Set: N:\CRF4\03242005\J527672.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:1462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22 after pos.:224 L:2167 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:40 after pos.:272